



## RESULT 2

A25732

Inhibin alpha chain precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A25732; S50897; A30161; A61548

C:Source: R.G.; Rung, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.; R.

Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986

A:Title: Cloning and sequence analysis of cDNA sequences coding for the two subunits of in

A:Reference number: A94097; MUID:86205842; PMID:3458167

A:Accession: A25732

A:Molecule type: mRNA

A:Residues: 1-360 &lt;FOR&gt;

A:Cross-references: GB:M13273; NID:q163194; PIDN:AA57414.1; PID:q163195

A:Note: part of this sequence, including the amino end of the mature protein, was confir

But, J. Biochem. 226, 751-764, 1994

But, J. Biochem. 226, 751-764, 1994

A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B

y DNase I footprinting.

A:Reference number: S50897; MUID:95112839; PMID:7813465

A:Accession: S50897

A:Molecule type: DNA

A:Residues: 1-87 &lt;THO&gt;

A:Cross-references: EMBL:U16237; NID:q563744; PIDN:AA60262.1; PID:q563745

R. Sugino, K.; Nakamura, T.; Takio, K.; Titani, K.; Miyamoto, K.; Hasegawa, Y.; Igarashi,

Biochem. Biophys. Res. Commun. 159, 1323-1329, 1989

A:Title: Inhibin alpha-subunit monomer is present in bovine follicular fluid.

A:Reference number: A30161; MUID:89193729; PMID:2530562

A:Accession: A30161

A:Molecule type: protein

A:Residues: 18-37:227-246 &lt;SUC&gt;

R. Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Matsuo,

Mol. Cell. Endocrinol. 44, 55-60, 1986

A:Title: Isolation of bovine follicular fluid inhibin of about 32 KDa.

A:Reference number: A61548; MUID:86136989; PMID:3081385

A:Accession: A61548

A:Molecule type: protein

A:Residues: 227-230 &lt;PUK&gt;

C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.

C:Superfamily: Inhibin

C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

F:1-17/Domain: signal sequence #status predicted &lt;SIG&gt;

F:18-226/Domain: propeptide #status predicted &lt;PRO&gt;

F:227-360/Product: inhibin alpha chain #status predicted &lt;MAT&gt;

F:140,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.4% Score 135; DB 1; Length 360;  
 Best Local Similarity 92.0%; Pred. No. 2, 9e-11;  
 Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 PWSPALRLQRPPEPAHACHR 25  
 Db 234 PWSPALRLQRPPEPAHACHR 258

RESULT 3  
 WEPGA

Inhibin alpha chain precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 18-Jun-1999

C:Accession: A01392; A25947

R. Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Deno, N.; Ying, S.Y.; Guillemin, R.;

Nature 318, 659-663, 1985

A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor

A:Reference number: A93371; MUID:86092207; PMID:2417121

A:Accession: A01392

A:Molecule type: mRNA

A:Residues: 1-364 &lt;MAS&gt;

A:Cross-references: GB:X03265; NID:q1999; PIDN:CAA27019.1; PID:q2000

R. Mayo, K.E.; Cerelli, G.M.; Spess, J.; Rivier, J.; Rosenfeld, M.G.; Evans, R.M.; Vale,

Proc. Natl. Acad. Sci. U.S.A. 83, 5849-5853, 1986

A:Title: Inhibin A-subunit cDNAs from porcine ovary and human placenta.

A:Reference number: A94116; MUID:86287350; PMID:3016724

A:Accession: A25947

A:Molecule type: mRNA

A:Residues: 1-119,'R',121-124,'A',126-364 &lt;MAT&gt;

A:Cross-references: GB:M1980; NID:q164518; PIDN:AA31057.1; PID:q164519

C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep

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OY 1 PMSPALRLQRPPEPAHANCHR 25  
|||||  
Db 241 PMSPALRLQRPPEPAHANCHR 265

## RESULT 5

A40056  
inhibin alpha chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A41398; A40056; A40905  
R: Feng, Z.M.; Li, Y.P.; Chen, C.L.C.  
Mol. Endocrinol. 3, 1914-1925, 1989  
A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit genes  
A:Reference number: A41398; MUID:90190649; PMID:2628729  
A:Accession: A41398  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-366 <F&N>  
A:Cross-references: GB:M2754; GB:M2755; NID:g204939; PIDN:AAA41437.1; PID:g204941  
R: Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsieh, A.J.W.; Mayo, K.E.  
Mol. Endocrinol. 1, 561-568, 1987  
A:Title: Rat inhibin: molecular cloning of alpha- and beta-subunit complementary deoxyri-  
A:Reference number: A40056; MUID:91042598; PMID:3153478  
A:Accession: A40056  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-366 <W00>  
A:Cross-references: GB:M6453; NID:g204934; PIDN:AAA41435.1; PID:g204935  
R: Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.U.; Ying, S.Y.; Ueno, N.  
Mol. Endocrinol. 1, 388-396, 1987  
A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of  
A:Reference number: A40905; MUID:9031931; PMID:2484214  
A:Accession: A40905  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-366 <ESC>  
A:Superfamily: inhibin  
C:Superfamily: inhibin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-23/Domain: propeptide #status predicted <PRO>  
F:234-366/Product: inhibin alpha chain #status predicted <MAT>  
F:147/269/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 89.5%; Score 128; DB 1; Length 366;  
Best local similarity 88.0%; Pred. No. 2.8e-10;  
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 PMSPALRLQRPPEPAHANCHR 25  
|||||  
Db 241 PMSPALRLQRPPEPAHANCHR 265

## RESULT 6

I51215  
inhibin alpha-subunit precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: I51215  
R: Wang, S.Y.; Johnson, P.A.  
Biol. Reprod. 49, 453-458, 1993  
A:Title: Complementary deoxyribonucleic acid cloning and sequence analysis of the alpha-  
A:Reference number: I51215; MUID:94002740; PMID:8399835  
A:Accession: I51215  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <W&N>  
A:Cross-references: GB:S65963; NID:g430815; PID:g430816  
C:Superfamily: inhibin

Query Match 70.6%; Score 101; DB 2; Length 328;  
Best local similarity 72.0%; Pred. No. 1.5e-06;  
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 PMSPALRLQRPPEPAHANCHR 25  
|||||  
Db 219 PMSPALRLQRPPEPAHANCHR 243

## RESULT 7

S61238  
hypothetical protein - bovine herpesvirus 1  
C:Species: bovine herpesvirus 1  
C:Date: 18-Sep-1997 #sequence\_revision 18-Sep-1997 #text\_change 26-Aug-1999  
C:Accession: S61238  
R: Vilek, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.  
submitted to the EMBL Data Library, January 1995  
A:Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesv-  
A:Reference number: S61233  
A:Accession: S61238  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-735 <VLC>  
A:Cross-references: EMBL:Z48053; NID:g971311; PIDN:CAA88116.1; PID:g971317  
C:Genetics:  
A:Introns: 341/3  
C:Superfamily: herpesvirus 38k protein

Query Match 39.2%; Score 56; DB 2; Length 735;  
Best local similarity 55.0%; Pred. No. 6.3;  
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
OY 5 SALRLQRPPEPAHANCHR 24  
|||||  
Db 116 SALRLQRPPEPAHANCHR 135

## RESULT 8

T09236  
nifz protein - Frankia alni  
C:Species: Frankia alni  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T09236  
R: Benson, D.R.  
submitted to the EMBL Data Library, November 1998  
A:Reference number: Z16624  
A:Accession: T09236  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-192 <F&N>  
A:Cross-references: EMBL:L29299; NID:g3953454; PID:g497435  
A:Experimental source: strain cp11  
C:Genetics:  
A:Gene: nifz  
C:Keywords: nitrogen fixation

Query Match 35.0%; Score 50; DB 2; Length 192;  
Best local similarity 31.4%; Pred. No. 11;  
Matches 11; Conservative 6; Mismatches 4; Indels 14; Gaps 1;  
OY 3 SPALRLQRPPEPAHANCHR 23  
|||||  
Db 102 APAAVLAEKVPAPPAHAGCAKCKHGSANC 136

## RESULT 9

J04207  
nitrogenase NifZ chain - Frankia sp.  
N:Alternate names: NifZ protein  
C:Species: Frankia sp.  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 22-Oct-1999  
C:Accession: J04207  
R: Harriott, O.T.; Hosted, T.J.; Benson, D.R.  
Gene 161, 63-67, 1995  
A:Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fi-  
A:Reference number: J04203; MUID:95369734; PMID:7642138

A:Accession: J04207  
 A:Molecule type: DNA  
 A:Residues: 1-192 <HAR>  
 A:Cross-references: GB:U29299; NID:q497430; PIDN:AAC02974.1; PID:q497435  
 C:Comment: This protein has an Ala and Pro rich region at its carboxyl-terminal region.  
 C:Genetics:  
 A:Gene: nifZ  
 C:Keywords: nitrogen fixation

Query Match 35.0%; Score 50; DB 2; Length 192;  
 Best Local Similarity 31.4%; Pred. No. 11;  
 Matches 11; Conservative 6; Mismatches 4; Indels 14; Gaps 1;

QY 3 SPSALRLQRPPEPAH-----ANNC 23  
 DB 102 APRAVVAEKVPAPPAHAGCAATCKHGSANC 136

RESULT 10  
 E83800  
 hypothetical protein BH1205 [imported] - Bacillus halodurans (strain C-125)  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C:Accession: E83800  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Cross-references: CH:AP001511; GB:BA000004; NID:q1017727; PIDN:BAB04924.1; GSPDB:GNOC  
 C:Genetics:  
 A:Experimental source: strain C-125  
 A:Gene: BH1205

Query Match 35.0%; Score 50; DB 2; Length 365;  
 Best Local Similarity 61.1%; Pred. No. 22;  
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 WSPSALRLQRPPEPAH 19  
 DB 324 WSGGTRLLQRDEGEAGA 341

RESULT 11  
 S35272  
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - carrot  
 C:Species: Daucus carota (carrot)  
 C:Date: 10-Dec-1993 #sequence\_revision 19-Jan-1996 #text\_change 18-Jun-1999  
 C:Accession: S35272; S32242  
 R:Luo, M.; Piffanelli, P.; Rastelli, L.; Cella, R.  
 Plant Mol. Biol. 22, 427-435, 1993  
 A:Title: Molecular cloning and analysis of a cDNA coding for the bifunctional dihydrofo  
 A:Reference number: S35272; MUID:93320381; PMID:8329682  
 A:Accession: S35272  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-528 <UD0>  
 A:Cross-references: EMBL:217306; NID:q288614; PIDN:CA78954.1; PID:q288615  
 C:Superfamily: bifunctional dihydrofolate reductase-thymidylate synthase; thymidylate sy  
 C:Keywords: methyltransferase; NADP; oxidoreductase  
 F:23-146/Domain: type I dihydrofolate reductase homology <Dfr>  
 F:244-528/Domain: thymidylate synthase homology <TDS>

Query Match 35.0%; Score 50; DB 2; Length 528;  
 Best Local Similarity 43.5%; Pred. No. 31;  
 Matches 10; Conservative 2; Mismatches 3; Indels 8; Gaps 1;

QY 2 WSPSALRLQRPPEPAHANCH 24  
 DB 396 WNPSDLRLMALP-----CH 410

RESULT 12  
 T14315  
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - carrot

N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)  
 C:Species: Daucus carota (carrot)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: T14315; S49321  
 R:Luo, M.; Piffanelli, P.; Rastelli, L.; Cella, R.  
 Plant Mol. Biol. 22, 427-435, 1993

A:Title: Molecular cloning and analysis of a cDNA coding for the bifunctional dihydro  
 A:Reference number: S35272; MUID:93320381; PMID:8329682  
 A:Accession: T14315

A:Status: preliminary; translated from uc/EMBL/DDBJ  
 A:Molecule type: DNA

A:Residues: 1-577 <UD0>

A:Cross-references: EMBL:AJ001135; NID:q3097055; PIDN:CA05895.1; PID:q3097056

R:Luo, M.; Orsi, R.; Cella, R.

Submitted to the EMBL Data Library, May 1994

A:Description: Plastidial localization of the bifunctional dihydrofolate reductase-1

A:Reference number: S49321

A:Accession: S49321

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-49 <UD0>

A:Cross-references: EMBL:233383; NID:q456699; PID:q556700

C:Genetics:

A:Note: DHFR-TS

C:Function:

A:Description: bifunctional enzyme catalyzes the reduction of folate into tetrahydro

rt of the enzyme

A:Note: bifunctional enzyme in plants and protozoan

C:Superfamily: bifunctional dihydrofolate reductase-thymidylate synthase; thymidylate

C:Keywords: methyltransferase; multifunctional enzyme; NADP; oxidoreductase

F:72-195/Domain: type I dihydrofolate reductase homology <Dfr>

F:293-577/Domain: thymidylate synthase homology <TDS>

Query Match 35.0%; Score 50; DB 2; Length 577;  
 Best Local Similarity 43.5%; Pred. No. 34;  
 Matches 10; Conservative 2; Mismatches 3; Indels 8; Gaps 1;

QY 2 WSPSALRLQRPPEPAHANCH 24  
 DB 445 WNPSDLRLMALP-----CH 459

RESULT 13  
 I52277  
 platelet-derived growth factor A-chain (novel form) - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C:Accession: I52277  
 R:Peng, L.; Xia, Y.; Tang, W.W.; Wilson, C.B.  
 Biochem. Biophys. Res. Commun. 194, 1453-1459, 1993  
 A:Title: Cloning a novel form of rat PDGF-A-chain with a unique 5' UT: regulation d  
 A:Reference number: I52277; MUID:93356827; PMID:8352804  
 A:Accession: I52277  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-63 <RES>  
 A:Cross-references: GB:S64566; NID:q404583

Query Match 34.3%; Score 49; DB 2; Length 63;  
 Best Local Similarity 42.9%; Pred. No. 5.2;  
 Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 WSPSALRLQRPPEPAHANCH 22  
 DB 38 WNPSCARLERPASPCHAS 58

## RESULT 14

S28721

hypothetical protein 1 - Trypanosoma brucei retrotransposon-like element TRS 1.6

C:Species: Trypanosoma brucei

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999

C:Accession: S28721

R:Murphy, N.B.; Pays, A.; Tebabi, P.; Coquelet, H.; Guyaux, M.; Pays, E.

J. Mol. Biol. 195, 855-871, 1987

A:Title: Trypanosoma brucei repeated element with unusual structural and transcriptional

A:Reference number: S28721; MUID:88011293; PMID:3656436

A:Accession: S28721

A:Molecule type: DNA

A:Residues: 1-1650 &lt;MUR&gt;

A:Cross-references: EMBL:X05710

A:Note: The authors translated the codon CAG for residue 1436 as Glu, CTC for residue 15

C:Genetics:

A:Mobile element: retrotransposon-like element TRS 1.6

A:Start codon: TIG

A:Introns: 627/3

## Query Match

34.3%; Score 49; DB 2; Length 1650;

Best Local Similarity 33.3%; Pred. No. 1.3e+02;

Matches 8; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 WSPSARLLQRPPEPPAAHANCHR 25

| | : : | | : | | |

DB 1153 WFDIIVAKRKPSSEVHENTR 1176

## RESULT 15

T14328

protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, GM1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T14328

R:Wright, M.R.; Hugo, C.; Seifert, R.; Distech, C.M.; Bowen-Pope, D.F.

J. Biol. Chem. 273, 23929-23937, 1998

A:Title: Proliferating and migrating mesangial cells responding to injury express a novel

A:Reference number: Z17986; MUID:98395110; PMID:9727007

A:Accession: T14328

A:Status: Preliminary; translated from CB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2302 &lt;WRI&gt;

A:Cross-references: EMBL:AF063249; NID:g93300095; P1D:g93300096; P1DN:AMC34801.1

A:Experimental source: Strain Wistar

C:Genetics:

A:Note: PTPRO

C:Keywords: phosphoric monoester hydrolase

F:1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F:19-2302/Product: protein-tyrosine phosphatase receptor type, GM1 #status predicted &lt;K

## Query Match

34.3%; Score 49; DB 2; Length 2302;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 SPSARLLQRPPEP 17

| | | | | | | | | |

DB 680 SPSRLKLSPEKP 694

Search completed: March 13, 2003, 13:59:33  
Job time : 22.5 secs